



SEQUENCE LISTING

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Wei, Bo

<120> DSP-15 DUAL-SPECIFICITY PHOSPHATASE

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<141> 2001-09-18

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Ala	Ile	Ser	Phe	Ile	Asp	Glu	Ala	Arg	Gly	Lys	Asn	Cys	Gly	Val	Leu
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Val	His	Cys	Leu	Ala	Gly	Ile	Ser	Arg	Ser	Val	Thr	Val	Thr	Val	Ala
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Val	His	Cys	Leu	Ala	Gly	Val	Ser	Arg	Ser	Val	Thr	Val	Thr	Val	Ala
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Leu	Met	Thr	Gln	Asn	Gly	Ile	Ser	Tyr	Val	Leu	Asn	Ala	Ser	Asn	Ser	
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Cys	Pro	Lys	Pro	Asp	Phe	Ile	Cys	Glu	Ser	Arg	Phe	Met	Arg	Val	Pro	
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Lys	Asp	Arg	Arg	Pro	Ser	Ile	Ser	Pro	Asn	Phe	Asn	Phe	Leu	Gly	Gln	
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Ser	Phe	Ile	Asp	Ser	Val	Lys	Asn	Ser	Gly	Gly	Arg	Val	Leu	Val	His	
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Gln	Arg	Arg	Gly	Val	Ile	Ser	Pro	Asn	Phe	Ser	Phe	Met	Gly	Gln	Leu
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Glu	Asp	Asn	His	Lys	Ala	Asp	Ile	Ser	Ser	Trp	Phe	Asn	Glu	Ala	Ile
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Asp	Phe	Ile	Asp	Ser	Ile	Lys	Asn	Ala	Gly	Gly	Arg	Val	Phe	Val	His
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Cys	Gln	Ala	Gly	Ile	Ser	Arg	Ser	Ala	Thr	Ile	Cys	Leu	Ala	Tyr	Leu
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Cys	Pro	Asn	His	Phe	Glu	Gly	His	Tyr	Gln	Tyr	Lys	Cys	Ile	Pro	Val
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Glu	Tyr	Ile	Asp	Ala	Val	Lys	Asp	Cys	Arg	Gly	Arg	Val	Leu	Val	His
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Cys	Gln	Ala	Gly	Ile	Ser	Arg	Ser	Ala	Thr	Ile	Cys	Leu	Ala	Tyr	Leu
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Met	Met	Lys	Lys	Arg	Val	Arg	Leu	Glu	Glu	Ala	Phe	Glu	Phe	Val	Lys
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Thr Ser Glu Ala Cys Met Thr His Leu His Tyr Lys Trp Ile Pro Val	
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Glu Asp Ser His Thr Ala Asp Ile Ser Ser His Phe Gln Glu Ala Ile	
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Asp Phe Ile Asp Cys Val Arg Glu Lys Gly Gly Lys Val Leu Val His	
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Cys Glu Ala Gly Ile Ser Arg Ser Pro Thr Ile Cys Met Ala Tyr Leu	
100 105 110	
Met Lys Thr Lys Gln Phe Arg Leu Lys Glu Ala Phe Asp Tyr Ile Lys	
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Arg Ser Phe Met His Val Asn Thr Asn Ala Asn Phe Tyr Lys Asp Ser	
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Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe Asn	
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Ala Gln Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr Ser	
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 Thr His Arg Phe Ile Glu Ala Ala Arg Ala Gln Gly Thr His Val Leu
 65 70 75 80
 Val His Cys Lys Met Gly Val Ser Arg Ser Ala Ala Thr Val Leu Ala
 85 90 95
 Tyr Ala Met Lys Gln Tyr Glu Cys Ser Leu Glu Gln Ala Leu Arg His
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Ala	Arg	Glu	Asn	Asn	Phe	Tyr	Ala	Ser	Gly	Pro	Ser	His	Asp	Trp	Leu
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Ser	Ser	Tyr	Glu	Arg	Arg	Ile	Glu	Ser	Asp	Gln	Ser	Cys	Leu	Asn	Glu
225				230					235						240
Trp	Asn	Ala	Met	Asp	Ala	Leu	Glu	Ser	Arg	Arg	Pro	Pro	Ser	Pro	Asp
				245					250					255	
Ala	Ile	Arg	Asn	Lys	Pro	Pro	Glu	Lys	Glu	Glu	Thr	Glu	Ser	Val	Ile
			260					265					270		
Lys	Met	Lys	Leu	Lys	Ala	Ile	Met	Met	Ser	Val	Asp	Leu	Asp	Glu	Val
		275					280					285			
Thr	Ser	Lys	Tyr	Ile	Arg	Gly	Arg	Leu	Glu	Glu	Ile	Leu	Asp	Met	Asp
	290					295					300				
Leu	Gly	Glu	Tyr	Lys	Ser	Phe	Ile	Asp	Ala	Glu	Met	Leu	Val	Ile	Leu
305					310					315					320
Gly	Gln	Met	Asp	Ala	Pro	Thr	Lys	Ile	Phe	Glu	His	Val	Tyr	Leu	Gly
			325						330					335	
Ser	Glu	Trp	Asn	Ala	Ser	Asn	Leu	Glu	Glu	Leu	Gln	Lys	Asn	Gly	Val
			340					345					350		
Arg	His	Ile	Leu	Asn	Val	Thr	Arg	Glu	Ile	Asp	Asn	Phe	Phe	Pro	Gly
		355					360					365			
Thr	Phe	Glu	Tyr	Phe	Asn	Val	Arg	Val	Tyr	Asp	Asp	Glu	Lys	Thr	Asn
	370				375						380				
Leu	Leu	Lys	Tyr	Trp	Asp	Asp	Thr	Phe	Arg	Tyr	Ile	Thr	Arg	Ala	Lys
385					390					395					400
Ala	Glu	Gly	Ser	Lys	Val	Leu	Val	His	Cys	Lys	Met	Gly	Val	Ser	Arg
			405						410					415	
Ser	Ala	Ser	Val	Val	Ile	Ala	Tyr	Ala	Met	Lys	Ala	Tyr	Gln	Trp	Glu
			420					425					430		
Phe	Gln	Gln	Ala	Leu	Glu	His	Val	Lys	Lys	Arg	Arg	Ser	Cys	Ile	Lys
	435					440						445			
Pro	Asn	Lys	Asn	Phe	Leu	Asn	Gln	Leu	Glu	Thr	Tyr	Ser	Gly	Met	Leu
	450					455					460				
Asp	Ala	Met	Lys	Asn	Lys	Glu	Lys	Leu	Gln	Arg	Ser	Lys	Ser	Glu	Thr
465				470					475						480
Asn	Leu	Lys	Ser	Thr	Lys	Asp	Ala	Arg	Leu	Leu	Pro	Gly	Ser	Glu	Pro
			485						490					495	
Thr	Pro	Leu	Ile	Gln	Ala	Leu	Asn	Gln	Ala	Lys	Ser	Lys	Ser	Thr	Gly
			500					505					510		
Glu	Ala	Gly	Val	Thr	Pro	Asp	Gly	Glu	Glu	Glu	Asp	Gly	Ser	Arg	Met
	515					520					525				
His	Arg	Arg	Ser	Ile	Ala	Gln	Lys	Ser	Gln	Arg	Arg	Met	Val	Arg	Arg
	530				535					540					
Ser	Ser	Ser	Thr	Ser	Pro	Lys	Thr	Gln	Thr	Ala	Val	Val	Thr	Lys	Gln
545					550					555					560
Gln	Ser	Gln	Ser	Met	Glu	Asn	Leu	Thr	Pro	Glu	Arg	Ser	Val	Ala	Glu
			565					570						575	
Glu	Pro	Lys	Asn	Met	Arg	Phe	Pro	Gly	Ser	Asn	Gly	Glu	Asn	Tyr	Ser
			580					585					590		
Val	Thr	Gln	Asn	Gln	Val	Leu	His	Ile	Gln	Lys	His	Thr	Pro	Leu	Ser
		595					600					605			

Val	Arg	Thr	Arg	Ile	His	Asp	Leu	Glu	Ala	His	Arg	Ala	Asp	Gln	Leu
610						615					620				
Pro	Gln	Gln	Pro	Val	Trp	Thr	Ser	Leu	Thr	Lys	Leu	Ile	Thr	Gln	Thr
625					630					635					640
Ser	His	Leu	Gly	Lys	Ser	Val	Ser	Gly	Ser	Ser	Ser	Gly	Asn	Ile	Asp
				645					650					655	
Ser	Arg	Arg	Asp	Ser	Ser	Cys	Ser	Asp	Val	Phe	Ser	Ser	Gln	Val	Asp
			660					665					670		
Ser	Val	Phe	Ala	Lys	Asp	Glu	Gly	Glu	Lys	Arg	Gln	Arg	Arg	Lys	Thr
		675					680					685			
His	Ser	Trp	Thr	Glu	Ser	Leu	Gly	Pro	Ser	Gly	Gly	Ile	Val	Leu	Asp
690						695					700				
Pro	Thr	Pro	Gln	Gln	Gln	Lys	Gln	Gln	Ser	Asn	Ala	Ile	Leu	Arg	Pro
705					710					715					720
Arg	Gly	Thr	Arg	Gln	Arg	Glu	Leu	Pro	Ser	Arg	His	Ala	Ser	Trp	Gly
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Ser

<210> 14
 <211> 509
 <212> PRT
 <213> Homo sapiens

<400> 14

Met	Thr	Leu	Ser	Thr	Leu	Ala	Arg	Lys	Arg	Lys	Ala	Pro	Leu	Ala	Cys
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			20					25					30		
Ala	Val	Ile	Ser	Gln	Asn	Ala	Ile	Asn	Gln	Leu	Ile	Ser	Glu	Ser	Phe
		35					40					45			
Leu	Thr	Val	Lys	Gly	Ala	Ala	Leu	Phe	Leu	Pro	Arg	Gly	Asn	Gly	Ser
50					55						60				
Ser	Thr	Pro	Arg	Ile	Ser	His	Arg	Arg	Asn	Lys	His	Ala	Gly	Asp	Leu
65					70					75					80
Gln	Gln	His	Leu	Gln	Ala	Met	Phe	Ile	Leu	Leu	Arg	Pro	Glu	Asp	Asn
				85					90					95	
Ile	Arg	Leu	Ala	Val	Arg	Leu	Glu	Ser	Thr	Tyr	Gln	Asn	Arg	Thr	Arg
			100					105					110		
Tyr	Met	Val	Val	Val	Ser	Thr	Asn	Gly	Arg	Gln	Asp	Thr	Glu	Glu	Ser
		115					120					125			
Ile	Val	Leu	Gly	Met	Asp	Phe	Ser	Ser	Asn	Asp	Ser	Ser	Thr	Cys	Thr
130						135					140				
Met	Gly	Leu	Val	Leu	Pro	Leu	Trp	Ser	Asp	Thr	Leu	Ile	His	Leu	Asp
145					150					155					160
Gly	Asp	Gly	Gly	Phe	Ser	Val	Ser	Thr	Asp	Asn	Arg	Val	His	Ile	Phe
				165					170					175	
Lys	Pro	Val	Ser	Val	Gln	Ala	Met	Trp	Ser	Ala	Leu	Gln	Ser	Leu	His
			180					185					190		
Lys	Ala	Cys	Glu	Val	Ala	Arg	Ala	His	Asn	Tyr	Tyr	Pro	Gly	Ser	Leu
		195					200					205			
Phe	Leu	Thr	Trp	Val	Ser	Tyr	Tyr	Glu	Ser	His	Ile	Asn	Ser	Asp	Gln
210						215					220				
Ser	Ser	Val	Asn	Glu	Trp	Asn	Ala	Met	Gln	Asp	Val	Gln	Ser	His	Arg
225					230					235					240
Pro	Asp	Ser	Pro	Ala	Leu	Phe	Thr	Asp	Ile	Pro	Thr	Glu	Arg	Glu	Arg

				245					250					255			
Thr	Glu	Arg	Leu	Ile	Lys	Thr	Lys	Leu	Arg	Glu	Ile	Met	Met	Gln	Lys		
			260					265					270				
Asp	Leu	Glu	Asn	Ile	Thr	Ser	Lys	Glu	Ile	Arg	Thr	Glu	Leu	Glu	Met		
		275					280					285					
Gln	Met	Val	Cys	Asn	Leu	Arg	Glu	Phe	Lys	Glu	Phe	Ile	Asp	Asn	Glu		
	290					295				300							
Met	Ile	Val	Ile	Leu	Gly	Gln	Met	Asp	Ser	Pro	Thr	Gln	Ile	Phe	Glu		
305					310					315					320		
His	Val	Phe	Leu	Gly	Ser	Glu	Trp	Asn	Ala	Ser	Asn	Leu	Glu	Asp	Leu		
			325					330						335			
Gln	Asn	Arg	Gly	Val	Arg	Tyr	Ile	Leu	Asn	Val	Thr	Arg	Glu	Ile	Asp		
			340					345					350				
Asn	Phe	Phe	Pro	Gly	Val	Phe	Glu	Tyr	His	Asn	Ile	Arg	Val	Tyr	Asp		
		355					360					365					
Glu	Glu	Ala	Thr	Asp	Leu	Leu	Ala	Tyr	Trp	Asn	Asp	Thr	Tyr	Lys	Phe		
	370					375					380						
Ile	Ser	Lys	Ala	Lys	Lys	His	Gly	Ser	Lys	Cys	Leu	Val	His	Cys	Lys		
385					390					395					400		
Met	Gly	Val	Ser	Arg	Ser	Ala	Ser	Thr	Val	Ile	Ala	Tyr	Ala	Met	Lys		
			405						410					415			
Glu	Tyr	Gly	Trp	Asn	Leu	Asp	Arg	Ala	Tyr	Asp	Tyr	Val	Lys	Glu	Arg		
		420						425					430				
Arg	Thr	Val	Thr	Lys	Pro	Asn	Pro	Ser	Phe	Met	Arg	Gln	Leu	Glu	Glu		
		435					440					445					
Tyr	Gln	Gly	Ile	Leu	Leu	Ala	Ser	Phe	Leu	Gly	Leu	Ile	His	Gly	Gly		
	450					455					460						
Arg	Asp	Lys	Pro	Trp	Gly	Glu	Lys	Ser	Thr	Glu	Phe	Glu	Ser	Val	Asp		
465					470					475					480		
Leu	Val	Ser	Ile	Pro	Gly	Ser	Pro	Ser	Cys	Cys	Asn	Pro	Glu	Lys	Leu		
			485						490					495			
Leu	His	Ile	Ser	His	Pro	Tyr	Leu	Thr	Pro	Ser	Ile	Lys					
		500						505									

<210> 15
 <211> 552
 <212> PRT
 <213> Homo sapiens

<400> 15
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 35 40 45
 Cys Glu Val Ala Arg Arg His Asn Tyr Phe Pro Gly Gly Val Ala Leu
 50 55 60
 Ile Trp Ala Thr Tyr Tyr Glu Ser Cys Ile Ser Ser Glu Gln Ser Cys
 65 70 75 80
 Ile Asn Glu Trp Asn Ala Met Gln Asp Leu Glu Ser Thr Arg Pro Asp
 85 90 95
 Ser Pro Ala Leu Phe Val Asp Lys Pro Thr Glu Gly Glu Arg Thr Glu
 100 105 110
 Arg Leu Ile Lys Ala Lys Leu Arg Ser Ile Met Met Ser Gln Asp Leu
 115 120 125

Glu	Asn	Val	Thr	Ser	Lys	Glu	Ile	Arg	Asn	Glu	Leu	Glu	Lys	Gln	Met
130						135					140				
Asn	Cys	Asn	Leu	Lys	Glu	Leu	Lys	Glu	Phe	Ile	Asp	Asn	Glu	Met	Leu
145					150					155					160
Leu	Ile	Leu	Gly	Gln	Met	Asp	Lys	Pro	Ser	Leu	Ile	Phe	Asp	His	Leu
				165					170					175	
Tyr	Leu	Gly	Ser	Glu	Trp	Asn	Ala	Ser	Asn	Leu	Glu	Glu	Leu	Gln	Gly
			180					185					190		
Ser	Gly	Val	Asp	Tyr	Ile	Leu	Asn	Val	Thr	Arg	Glu	Ile	Asp	Asn	Phe
		195					200					205			
Phe	Pro	Gly	Leu	Phe	Ala	Tyr	His	Asn	Ile	Arg	Val	Tyr	Asp	Glu	Glu
210						215					220				
Thr	Thr	Asp	Leu	Leu	Ala	His	Trp	Asn	Glu	Ala	Tyr	His	Phe	Ile	Asn
225					230					235					240
Lys	Ala	Lys	Arg	Asn	His	Ser	Lys	Cys	Leu	Val	His	Cys	Lys	Met	Gly
				245					250					255	
Val	Ser	Arg	Ser	Ala	Ser	Thr	Val	Ile	Ala	Tyr	Ala	Met	Lys	Glu	Phe
			260					265					270		
Gly	Trp	Pro	Leu	Glu	Lys	Ala	Tyr	Asn	Tyr	Val	Lys	Gln	Lys	Arg	Ser
		275					280					285			
Ile	Thr	Arg	Pro	Asn	Ala	Gly	Phe	Met	Arg	Gln	Leu	Ser	Glu	Tyr	Glu
290						295					300				
Gly	Ile	Leu	Asp	Ala	Ser	Lys	Gln	Arg	His	Asn	Lys	Leu	Trp	Arg	Gln
305					310					315					320
Gln	Thr	Asp	Ser	Ser	Leu	Gln	Gln	Pro	Val	Asp	Asp	Pro	Ala	Gly	Pro
				325					330					335	
Gly	Asp	Phe	Leu	Pro	Glu	Thr	Pro	Asp	Gly	Thr	Pro	Glu	Ser	Gln	Leu
			340					345					350		
Pro	Phe	Leu	Asp	Asp	Ala	Ala	Gln	Pro	Gly	Leu	Gly	Pro	Pro	Leu	Pro
		355					360					365			
Cys	Cys	Phe	Arg	Arg	Leu	Ser	Asp	Pro	Leu	Leu	Pro	Ser	Pro	Glu	Asp
370						375					380				
Glu	Thr	Gly	Ser	Leu	Val	His	Leu	Glu	Asp	Pro	Glu	Arg	Glu	Ala	Leu
385					390					395					400
Leu	Glu	Glu	Ala	Ala	Pro	Pro	Ala	Glu	Val	His	Arg	Pro	Ala	Arg	Gln
				405					410					415	
Pro	Gln	Gln	Gly	Ser	Gly	Leu	Cys	Glu	Lys	Asp	Val	Lys	Lys	Lys	Leu
			420					425					430		
Glu	Phe	Gly	Ser	Pro	Lys	Gly	Arg	Ser	Gly	Ser	Leu	Leu	Gln	Val	Glu
		435					440					445			
Glu	Thr	Glu	Arg	Glu	Glu	Gly	Leu	Gly	Ala	Gly	Arg	Trp	Gly	Gln	Leu
450						455					460				
Pro	Thr	Gln	Leu	Asp	Gln	Asn	Leu	Leu	Asn	Ser	Glu	Asn	Leu	Asn	Asn
465					470					475					480
Asn	Ser	Lys	Arg	Ser	Cys	Pro	Asn	Gly	Met	Glu	Val	Gly	Arg	Ala	Arg
				485					490					495	
Pro	Ala	Gly	Trp	His	Thr	Pro	Ser	Leu	Pro	Ser	His	Ser	Asn	Trp	Pro
			500					505					510		
Thr	Ser	Ala	Ser	Val	Val	Gly	Thr	Thr	Gly	Thr	Arg	His	His	Thr	Gln
		515					520					525			
Leu	Ile	Phe	Phe	Tyr	Cys	Leu	Leu	Trp	Ala	Pro	Ser	Ser	His	Leu	Gln
530						535					540				
Gly	Pro	Glu	Gly	Ser	Phe	Thr	Gly								
545					550										

<211> 10
 <212> PRT
 <213> Homo sapiens

<400> 16
 Val His Cys Lys Met Gly Val Ser Arg Ser
 1 5 10

<210> 17
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Conserved homology region from eight DSPs having
 MAP-kinase phosphatase activity

<400> 17
 Asn Gly Arg Val Leu Val His Cys Gln Ala Gly Ile Ser Arg Ser Gly
 1 5 10 15
 Thr Asn Ile Leu Ala Tyr Leu Met
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<210> 18
 <211> 22
 <212> PRT
 <213> Homo sapiens

<400> 18
 Val Leu Val His Cys Lys Met Gly Val Ser Arg Ser Ala Ala Thr Val
 1 5 10 15
 Leu Ala Tyr Ala Met Lys
 20

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 19
 tgtcgatgaa gtcacggtac tgctggaggg 30

<210> 20
 <211> 1416
 <212> DNA
 <213> Mus musculus

<400> 20
 atggccctgg tcacagtgg ccgttcgccc ccgggcagcg gcgcctccac gcccggtggg 60
 ccctgggacc aggcggtcca gcgaaggagt cgactccagc gaaggcagag ctttgcggtg 120
 ctccgtgggg ctgtcctggg actgcaggat ggaggggaca atgatgatgc agcagaggcc 180

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agttctgagc caacagagaa ggccccgagt gaggaggagc tccacgggga ccagacagac 240
ttcgggcaag gatcccagag tccccagaag caggaggagc agaggcagca cctgcacctc 300
atggtacagc tgctgaggcc gcaggatgac atccgcctgg cagcccagct ggaggcaccc 360
cggcctcccc ggctccgcta cctgctggta gtttctacac gagaaggaga aggtctgagc 420
caggatgaga cggtcctcct gggcgtggat ttccctgaca gcagctcccc cagctgcacc 480
ctgggcctgg tcttgcccct ctggagtgac acccaggtgt acttagatgg agacgggggc 540
ttcagcgtga cgtctggtgg gcaaagccgg atcttcaagc ccatctccat ccagaccatg 600
tgggccacac tccaggtatt gcaccaagca tgtgaggcag ctctaggcag cggccttgta 660
ccgggtggca gtgccctcac ctgggccagc cactaccagg agagactgaa ctccgaacag 720
agctgcctca atgagtggac ggctatggcc gacctggagt ctctgcggcc tcccagcgcc 780
gagcctggcg ggtcctcaga acaggagcag atggagcagg cgatccgtgc tgagctgtgg 840
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gcggccacag tgctggccta tgccatgaag cagtacgaat gcagcctgga gcaggccctg 1320
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cagatctacc agggcatcct gacggccaga acctga 1416

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<210> 21
 <211> 471
 <212> PRT
 <213> Mus musculus

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<400> 21
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          20          25          30
Gln Arg Arg Gln Ser Phe Ala Val Leu Arg Gly Ala Val Leu Gly Leu
          35          40          45
Gln Asp Gly Gly Asp Asn Asp Asp Ala Ala Glu Ala Ser Ser Glu Pro
          50          55          60
Thr Glu Lys Ala Pro Ser Glu Glu Glu Leu His Gly Asp Gln Thr Asp
65          70          75          80
Phe Gly Gln Gly Ser Gln Ser Pro Gln Lys Gln Glu Glu Gln Arg Gln
          85          90          95
His Leu His Leu Met Val Gln Leu Leu Arg Pro Gln Asp Asp Ile Arg
          100          105          110
Leu Ala Ala Gln Leu Glu Ala Pro Arg Pro Pro Arg Leu Arg Tyr Leu
          115          120          125
Leu Val Val Ser Thr Arg Glu Gly Glu Gly Leu Ser Gln Asp Glu Thr
          130          135          140
Val Leu Leu Gly Val Asp Phe Pro Asp Ser Ser Ser Pro Ser Cys Thr
145          150          155          160
Leu Gly Leu Val Leu Pro Leu Trp Ser Asp Thr Gln Val Tyr Leu Asp
          165          170          175
Gly Asp Gly Gly Phe Ser Val Thr Ser Gly Gly Gln Ser Arg Ile Phe
          180          185          190
Lys Pro Ile Ser Ile Gln Thr Met Trp Ala Thr Leu Gln Val Leu His
          195          200          205
Gln Ala Cys Glu Ala Ala Leu Gly Ser Gly Leu Val Pro Gly Gly Ser
          210          215          220
Ala Leu Thr Trp Ala Ser His Tyr Gln Glu Arg Leu Asn Ser Glu Gln

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225		230		235		240									
Ser	Cys	Leu	Asn	Glu	Trp	Thr	Ala	Met	Ala	Asp	Leu	Glu	Ser	Leu	Arg
			245						250					255	
Pro	Pro	Ser	Ala	Glu	Pro	Gly	Gly	Ser	Ser	Glu	Gln	Glu	Gln	Met	Glu
			260					265						270	
Gln	Ala	Ile	Arg	Ala	Glu	Leu	Trp	Lys	Val	Leu	Asp	Val	Ser	Asp	Leu
		275					280					285			
Glu	Ser	Val	Thr	Ser	Lys	Glu	Ile	Arg	Gln	Ala	Leu	Glu	Leu	Arg	Leu
	290					295					300				
Gly	Leu	Pro	Leu	Gln	Gln	Tyr	Arg	Asp	Phe	Ile	Asp	Asn	Gln	Met	Leu
305					310					315					320
Leu	Leu	Val	Ala	Gln	Arg	Asp	Arg	Ala	Ser	Arg	Ile	Phe	Pro	His	Leu
			325						330					335	
Tyr	Leu	Gly	Ser	Glu	Trp	Asn	Ala	Ala	Asn	Leu	Glu	Glu	Leu	Gln	Arg
			340					345						350	
Asn	Arg	Val	Thr	His	Ile	Leu	Asn	Met	Ala	Arg	Glu	Ile	Asp	Asn	Phe
		355					360					365			
Tyr	Pro	Glu	Arg	Phe	Thr	Tyr	His	Asn	Val	Arg	Leu	Trp	Asp	Glu	Glu
	370					375					380				
Ser	Ala	Gln	Leu	Leu	Pro	His	Trp	Lys	Glu	Thr	His	Arg	Phe	Ile	Glu
385					390					395					400
Ala	Ala	Arg	Ala	Gln	Gly	Thr	His	Val	Leu	Val	His	Cys	Lys	Met	Gly
			405						410					415	
Val	Ser	Arg	Ser	Ala	Ala	Thr	Val	Leu	Ala	Tyr	Ala	Met	Lys	Gln	Tyr
			420					425					430		
Glu	Cys	Ser	Leu	Glu	Gln	Ala	Leu	Arg	His	Val	Gln	Glu	Leu	Arg	Pro
		435					440					445			
Ile	Ala	Arg	Pro	Asn	Pro	Gly	Phe	Leu	Arg	Gln	Leu	Gln	Ile	Tyr	Gln
	450					455					460				
Gly	Ile	Leu	Thr	Ala	Arg	Thr									
465					470										

<210> 22
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 22
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24

<210> 23
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 23
 gcgccagctg cagatctacc agggcat

27

<210> 24
 <211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
cactttccac agctcagcac ggatcgcc 28

<210> 25
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
cgcagagact ccaggctcggc catagcc 27

<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 26
ggggttgagg gaaggggccg tgc 23

<210> 27
<211> 6
<212> PRT
<213> Homo sapiens

<400> 27
Asp Ala Asp Glu Tyr Leu
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<210> 28
<211> 2718
<212> DNA
<213> Homo sapiens

<400> 28
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gcccccgggc agcggcgcct ccacgcccgt ggggccctgg gaccaggcgg tccagcgaag 120
gagtcgactc cagcgaaggc agagctttgc ggtgctcgt ggggctgtcc tgggactgca 180
ggatggaggg gacaatgatg atgcagcaga ggccagttct gagccaacag agaaggcccc 240
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